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Genome-wide expression analysis of reactive oxygen species gene network in Mizuna plants grown in long-term spaceflight

Sugimoto M., Oono Y., Gusev O., Matsumoto T., Yazawa T., Levinskikh M., Sychev V., Bingham G., Wheeler R., Hummerick M.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

Background: Spaceflight environment have been shown to generate reactive oxygen species (ROS) and induce oxidative stress in plants, but little is known about the gene expression of the ROS gene network in plants grown in long-term spaceflight. The molecular response and adaptation to the spaceflight environment of Mizuna plants harvested after 27 days of cultivation onboard the International Space Station (ISS) were measured using genome-wide mRNA expression analysis (mRNA-Seq). Results: Total reads of transcripts from the Mizuna grown in the ISS as well as on the ground by mRNA-Seq showed 8,258 and 14,170 transcripts up-regulated and down-regulated, respectively, in the space-grown Mizuna when compared with those from the ground-grown Mizuna. A total of 20 in 32 ROS oxidative marker genes were up-regulated, including high expression of four hallmarks, and preferentially expressed genes associated with ROS-scavenging including thioredoxin, glutaredoxin, and alternative oxidase genes. In the transcription factors of the ROS gene network, MEKK1-MKK4-MPK3, OXI1-MKK--MPK3, and OXI1-MPK3 of MAP cascades, induction of WRKY22 by MEKK1-MKK4-MPK3 cascade, induction of WRKY25 and repression of Zat7 by Zat12 were suggested. RbohD and RbohF genes were up-regulated preferentially in NADPH oxidase genes, which produce ROS. Conclusions: This large-scale transcriptome analysis revealed that the spaceflight environment induced oxidative stress and the ROS gene network activation in the space-grown Mizuna. Among transcripts altered in expression by space conditions, some were common genes response to abiotic and biotic stress. Furthermore, certain genes were exclusively up-regulated in Mizuna grown on the ISS. Surprisingly, Mizuna grew in space normally, as well as on the ground, demonstrating that plants can acclimate to long-term exposure in the spaceflight environment by reprogramming the expression of the ROS gene network. © 2014 Sugimoto et al.; licensee BioMed Central Ltd.

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Keywords

International Space Station, Mizuna, mRNA-Seq, Next generation sequencing, Reactive oxygen species, Spaceflight, Transcriptome